Amendments to the Specification:

On page 31, please amend the paragraph at lines 13-16 as follows.

- Figure 2 ~~Figures 2B-2H~~ schematically shows some examples of genetic constructs according to the invention containing reporter genes and ~~, with Figure 2A showing~~ the vector pBINI9^{PTT} used as the starting material for the construction of these genetic constructs.[[.]]

On page 38, please amend the paragraph at lines 29-32 as follows.

Schematic representations of some non-limiting examples of constructs of the invention are shown in Figure 2 ~~Figures 2B-2H~~. Instead of the luciferase gene shown in Figure 2, also another reporter gene such as (a sequence encoding a) beta- glucuronidase (GUS) can be used, or a sequence encoding the desired protein or polypeptide.

On page 39, please amend the paragraph at lines 1-19 as follows.

Briefly, the assembly of all constructs for potato transformation was started with the vector pBINI9^{PTT} (Fig. 2~~A~~), which already contained the tuber- specific GBSS I promoter, the amyloplast-targeting signal of potato GBSS 1, and the NOS terminator sequence (for legend see figure). The starch-binding modules SBD and GBSS were obtained by standard PCR using the cyclodextrin glycosyltransferase of *Bacillus circulans* and potato granule-bound starch synthase I as a template, respectively. The luciferase template (pLUK07/LUC) was obtained from the North Carolina State University. PCRs were performed in such a way that the appropriate restriction sites were introduced in the genes of interest. The relevant restriction sites are indicated in Figure 2. An artificial

linker sequence was designed, containing a BglII and an EcoRl restriction site at, respectively, the 5' and 3' end of the sequence. The amino acid sequence of the PT-rich linker peptide corresponds to "RSPTPTPTTPTPTPTTPTPTPSTE" (SEQ ID NO:5). The correctness of the constructs was confirmed by DNA sequencing. The constructs were introduced in both WT and amylose-free potato plants using standard *Agrobacterium*-mediated transformation procedures. The constructs provide the opportunity (i) to investigate whether SBD and GBSS bind the granule at a different location; (ii) to compare the affinity of SBD, SBD_2 and GBSS for starch during granule biosynthesis; (iii) to verify the concept of targeting foreign catalytic activities to the starch granule during biosynthesis.